```
=> s tuberculosis and
((MTSP1) or (MTSP15) or (MTSP21) or (MTSP23) or (MTSP36) or (MTSP43) or (MTSP47) or (Rv0603) or (Rv1804c) or (Rv12
71c) or (Rv2253) or (Rv0203) or (Rv0617) or (Rv2290))
L1          10 TUBERCULOSIS AND ((MTSP1) OR (MTSP15) OR (MTSP21) OR (MTSP23) OR (MT
               SP36) OR (MTSP43) OR (MTSP47) OR (RV0603) OR (RV1804C) OR (RV1271C)
               OR (RV2253) OR (RV0203) OR (RV0617) OR (RV2290))

=> dup rem l1
PROCESSING COMPLETED FOR L1
L2           6 DUP REM L1 (4 DUPLICATES REMOVED)

=> d bib ab 1-
YOU HAVE REQUESTED DATA FROM 6 ANSWERS - CONTINUE? Y/(N):y


L2     ANSWER 1 OF 6   USPATFULL on STN
AN     2005:305853  USPATFULL
TI     High resolution typing system for pathogenic Mycobacterium tuberculosum
IN     Keim, Paul S., Flagtaff, AZ, UNITED STATES
       Spurgiesz, Robert Scott, Flagstaff, AZ, UNITED STATES
       Schupp, James M., Flagstaff, AZ, UNITED STATES
PI     US 2005266492      A1    20051201
AI     US 2005-181587     A1    20050713 (11)
RLI    Division of Ser. No. US 2003-624714, filed on 21 Jul 2003, PENDING
PRAI   US 2002-397224P      20020719 (60)
DT     Utility
FS     APPLICATION
LREP   QUARLES & BRADY LLP, RENAISSANCE ONE, TWO NORTH CENTRAL AVENUE, PHOENIX,
       AZ, 85004-2391, US
CLMN   Number of Claims: 23
ECL    Exemplary Claim: 1
DRWN   3 Drawing Page(s)
LN.CNT 1244
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB     MLVA methods for strain discrimination among Mycobacterium tuberculosum
       strains are disclosed. Nine VNTR loci have been identified from genomic
       sequences of Mycobacterium tuberculosum strains and primer pairs
       suitable for amplifying the VNTR by PCR are disclosed. Polymorphisms at
       these loci were used to resolve genotypes into distinct groups. This
       sub-typing scheme is useful for the epidemiological study of
       Mycobacterium tuberculosum and may be applied to the local detection of
       the pathological causative agent of tuberculosum.

L2     ANSWER 2 OF 6  CAPLUS   COPYRIGHT 2005 ACS on STN
AN     2005:11168   CAPLUS
DN     142:234084
TI     Cloning and expression of multiple integral membrane proteins from
       Mycobacterium tuberculosis in Escherichia coli
AU     Korepanova, Alla; Gao, Fei P.; Hua, Yuanzi; Qin, Huajun; Nakamoto, Robert
       K.; Cross, Timothy A.
CS     Department of Chemistry and Biochemistry, Florida State University,
       Tallahassee, FL, 32306, USA
SO     Protein Science (2005), 14(1), 148-158
       CODEN: PRCIEI; ISSN: 0961-8368
PB     Cold Spring Harbor Laboratory Press
DT     Journal
LA     English
AB     Seventy integral membrane proteins from the Mycobacterium
       tuberculosis genome have been cloned and expressed in Escherichia
       coli. A combination of T7 promoter-based vectors with hexa-His affinity
       tags and BL21 E. coli strains with addnl. tRNA genes to supplement
       sparsely used E. coli codons have been most successful. The expressed
       proteins have a wide range of mol. wts. and number of transmembrane helixes.
       Expression of these proteins has been observed in the membrane and insol.
       fraction of E. coli cell lysates and, in some cases, in the soluble fraction.
       The highest expression levels in the membrane fraction were restricted to
       a narrow range of mol. wts. and relatively few transmembrane helixes. In
       contrast, overexpression in insol. aggregates was distributed over a broad
       range of mol. wts. and number of transmembrane helixes.
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L2   ANSWER 3 OF 6 BIOSIS   COPYRIGHT (c) 2005 The Thomson Corporation   on STN
      DUPLICATE 1
AN   2005:167656 BIOSIS
DN   PREV200500169558
TI   Immunological characterization of novel secreted antigens of Mycobacterium
      tuberculosis.
AU   Amor, Y. B.; Shashkina, E.; Johnson, S.; Bifani, P. J.; Kurepina, N.;
      Kreiswirth, B.; Bhattacharya, S.; Spencer, J.; Rendon, A.; Catanzaro, A.;
      Gennaro, M. L. [Reprint Author]
CS   225 Warren St, Newark, NJ, 07103, USA
      gennaro@phri.org
SO   Scandinavian Journal of Immunology, (February 2005) Vol. 61, No. 2, pp.
      139-146. print.
      ISSN: 0300-9475 (ISSN print).
DT   Article
LA   English
ED   Entered STN: 4 May 2005
      Last Updated on STN: 4 May 2005
AB   Proteins secreted by Mycobacterium **tuberculosis** are targets of
      host immune responses and as such are investigated for vaccine and
      immunodiagnostics development. Computer-driven searches of the M.
      tuberculosis H37Rv genome had previously identified 45 novel
      secreted proteins. Here, we report the characterization of these antigens
      in terms of specificity for the M. **tuberculosis** complex and the
      ability to induce human immune responses. BLAST homology searches and
      Southern hybridization identified 10 genes that were either specific for
      the M. **tuberculosis** complex or found in only two nontuberculous
      mycobacterial species of minor medical significance. Selected recombinant
      proteins were purified from Escherichia coli cells and tested for the
      ability to elicit antibody responses in **tuberculosis** patients.
      Reactivity of the serum panel was '36% with at least one of five novel
      proteins (**Rv0203, Rv0603, Rv1271c,**
      Rv1804c and **Rv2253**), 56% with the 38 kDa lipoprotein, a
      M. **tuberculosis** antigen known to be highly seroreactive, and 68%
      with a combination of **Rv0203, Rv1271c** and the 38 kDa
      antigen. Thus, at least five novel secreted proteins induce antibody
      responses during active disease; some of these proteins may increase the
      sensitivity of serological assays based on the 38 kDa antigen.

L2   ANSWER 4 OF 6 USPATFULL on STN
AN   2004:254370 USPATFULL
TI   Comparative mycobacterial geneomics as a tool for identifying targets
      for the diagnosis, prophylaxis or treatment of mycobacterioses
IN   Cole, Stewart, Clamart, FRANCE
PI   US 2004197896   A1   20041007
AI   US 2004-468356   A1   20040412 (10)
      WO 2002-IB1973   20020222
RLI   Division of Ser. No. US 2001-270123, filed on 22 Feb 2001, PENDING
DT   Utility
FS   APPLICATION
LREP FINNEGAN, HENDERSON, FARABOW, GARRETT & DUNNER, LLP, 1300 I STREET, NW,
      WASHINGTON, DC, 20005
CLMN Number of Claims: 50
ECL   Exemplary Claim: 1
DRWN 103 Drawing Page(s)
LN.CNT 2647
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB   The present invention is directed to a method of selection of purified
         nucleotidic sequences or polynucleotides encoding proteins or part of
         proteins carrying at least an essential function for the survival or the
         virulence of mycobacterium species by a comparative genomic analysis of
         the sequence of the genome of M. **tuberculosis** aligned on the
         genome sequence of M. leprae and M. **tuberculosis** and M. leprae
         marker polypeptides of nucleotides encoding the polypeptides, and
         methods for using the nucleotides and the encoded polypeptides are
         disclosed.

AN   2004:158567   USPATFULL
TI   High resolution typing system for pathogenic Mycobacterium tuberculosum
IN   Keim, Paul S., Flagstaff, AZ, UNITED STATES
        Spurgiesz, Robert Scott, Flagstaff, AZ, UNITED STATES
        Schupp, James M., Flagstaff, AZ, UNITED STATES
PI   US 2004121366   A1   20040624
AI   US 2003-624714   A1   20030721 (10)
PRAI   US 2002-397224P   20020719 (60)
DT   Utility
FS   APPLICATION
LREP   QUARLES & BRADY LLP, RENAISSANCE ONE, TWO NORTH CENTRAL AVENUE, PHOENIX,
        AZ, 85004-2391
CLMN   Number of Claims: 17
ECL   Exemplary Claim: 1
DRWN   3 Drawing Page(s)
LN.CNT 1061
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB   MLVA methods for strain discrimination among Mycobacterium tuberculosum
        strains are disclosed. Nine VNTR loci have been identified from genomic
        sequences of Mycobacterium tuberculosum strains and primer pairs
        suitable for amplifying the VNTR by PCR are disclosed. Polymorphisms at
        these loci were used to resolve genotypes into distinct groups. This
        sub-typing scheme is useful for the epidemiological study of
        Mycobacterium tuberculosum and may be applied to the local detection of
        the pathological causative agent of tuberculosum.

AN   2003:187811   USPATFULL
TI   Comparative mycobacterial genomics as a tool for identifying targets for
        the diagnosis, prophylaxis or treatment of mycobacterioses
IN   Cole, Stewart T., Clamart, FRANCE
PI   US 2003129601   A1   20030710
        US 2004121322   A9   20040624
AI   US 2002-80170   A1   20020222 (10)
PRAI   US 2001-270123P   20010222 (60)
DT   Utility
FS   APPLICATION
LREP   FINNEGAN, HENDERSON, FARABOW, GARRETT &, DUNNER LLP, 1300 I STREET, NW,
        WASHINGTON, DC, 20006
CLMN   Number of Claims: 74
ECL   Exemplary Claim: 1
DRWN   3 Drawing Page(s)
LN.CNT 6691
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB   The present invention is directed to a method of selection of purified
        nucleotidic sequences or polynucleotides encoding proteins or part of
        proteins carrying at least an essential function for the survival or the
        virulence of mycobacterium species by a comparative genomic analysis of
        the sequence of the genome of M. **tuberculosis** aligned on the
        genome sequence of M. leprae and M. **tuberculosis** and M. leprae
        marker polypeptides of nucleotides encoding the polypeptides, and
        methods for using the nucleotides and the encoded polypeptides are
        disclosed.